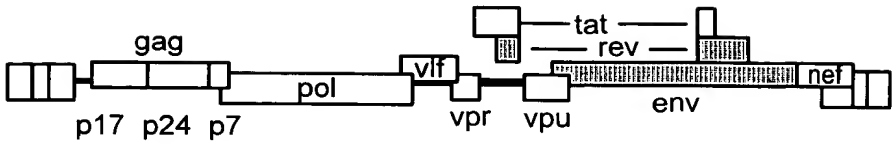



**Figure 1A**

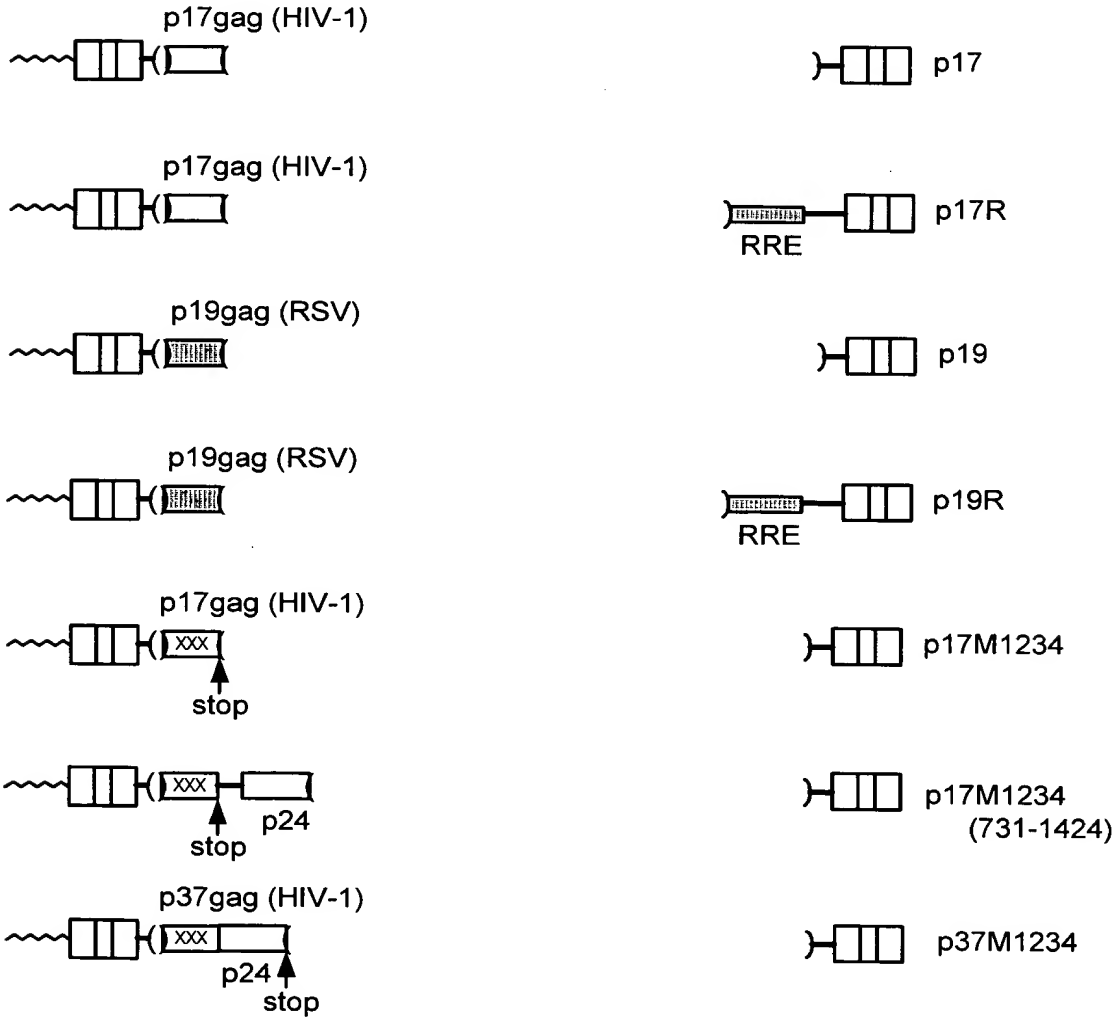



**Figure 1B**

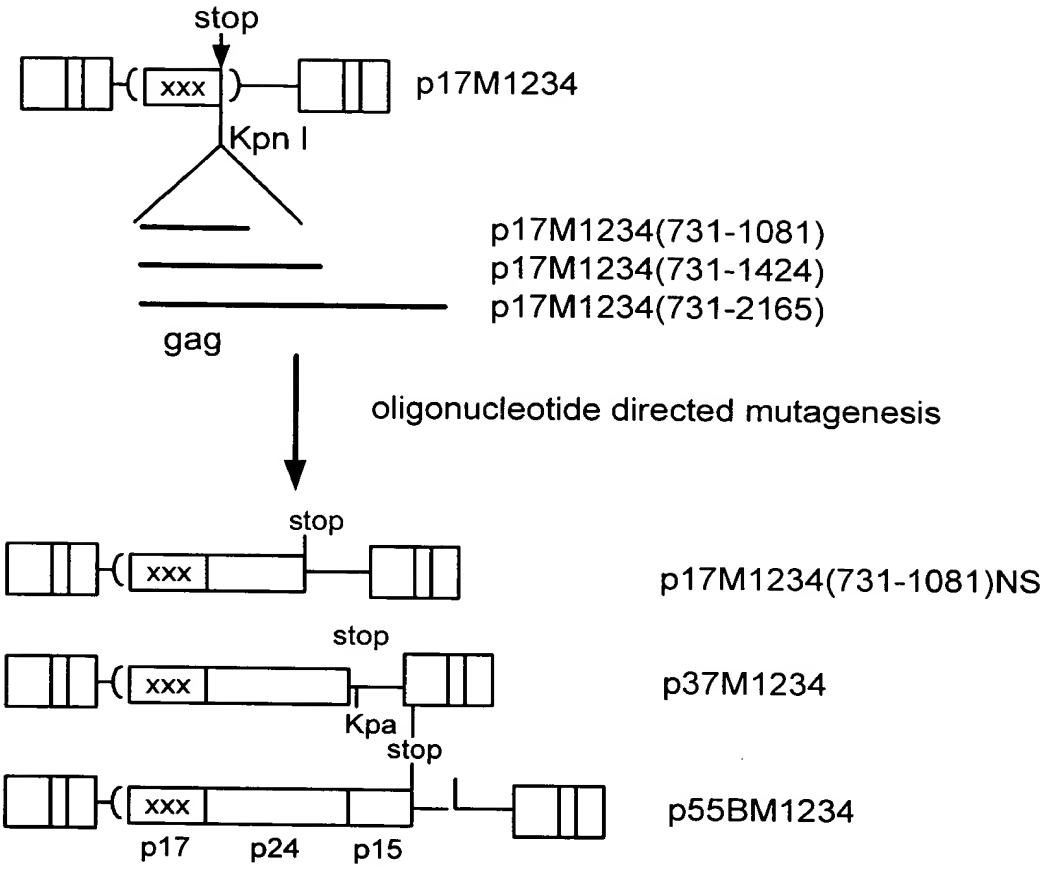
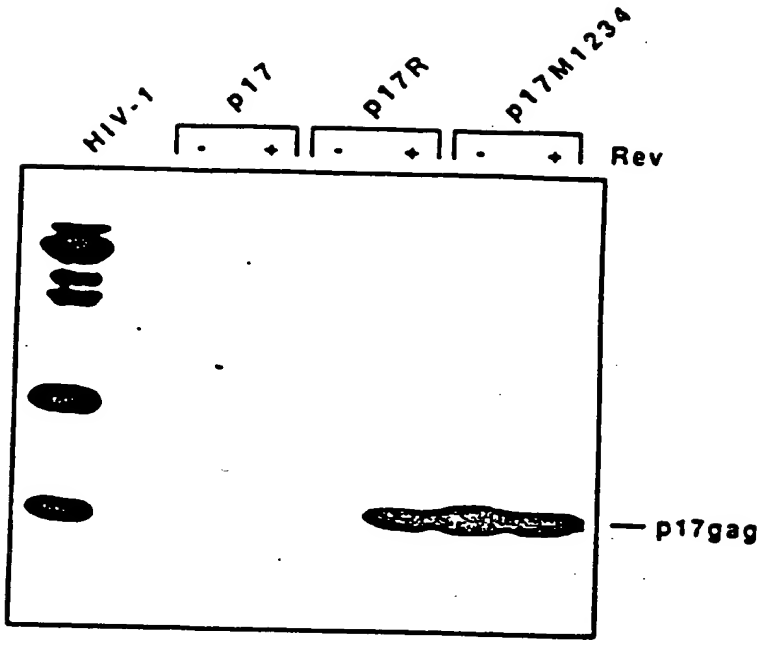



**Figure 1C**

A




B

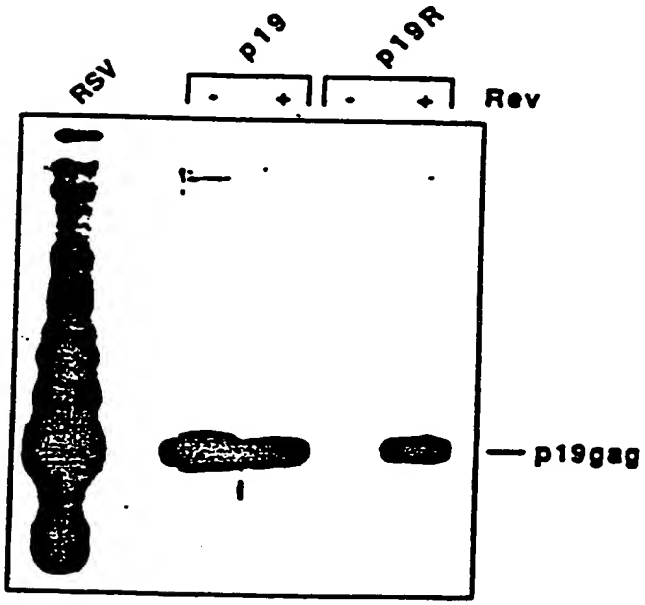
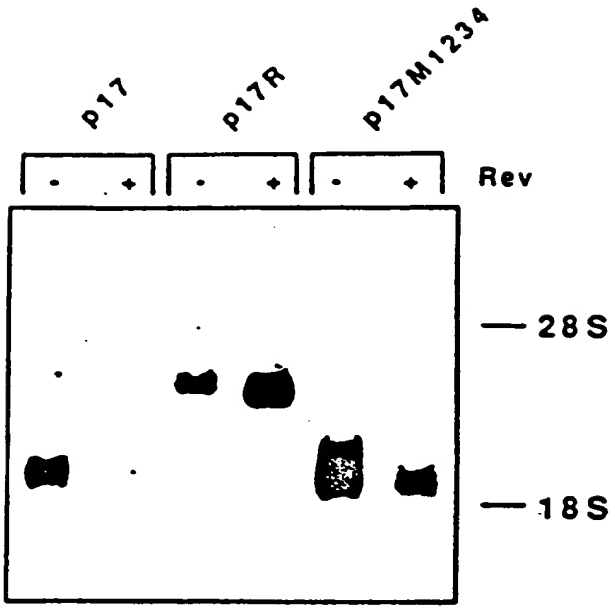



Figure 2

A




B

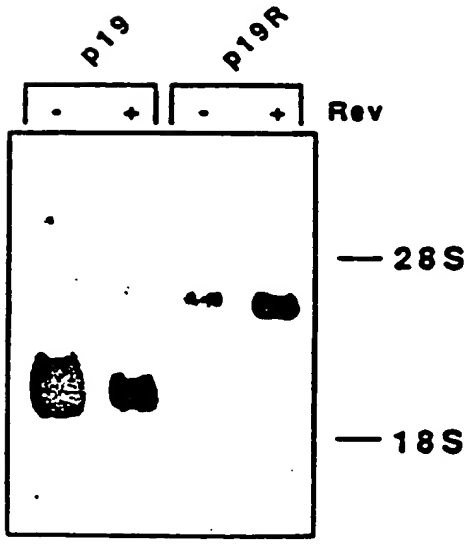



Figure 3

```
336
atg ggt gcg aga gcg tca gta tta agc ggg gga gaa tta gat cga tgg gaa aaa att cgg

396                                   M1
tta agg cca gcc gga aag aaa aaa tat aaa tta aaa cat ata gta tgg gca agc agg gag
                          G   G   C   G C     G   C   C
456
cta gaa cga ttc gca gtt aat cct ggc ctg tta gaa aca tca gaa ggc tgt aga caa ata

516                                                   M2
ctg gga cag cta caa cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat
                                                      G   G     C       C     C   C
576                                   M3
aca gta gca acc ctc tat tgt gtg cat caa agg ata gag ata aaa gac acc aag gaa gct
                                  C   G C     C       C   G
636                                       M4
tta gac aag ata gag gaa gag caa aac aaa agt aag aaa aaa gca cag caa gca gca gct
                                  G TCC       G   G   C       G
696
gac aca gga cac agc aat cag gtc agc caa aat tac
```

**Figure 4**

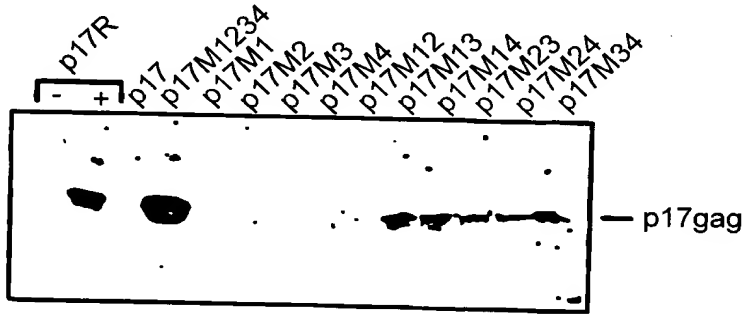



**Figure 5**

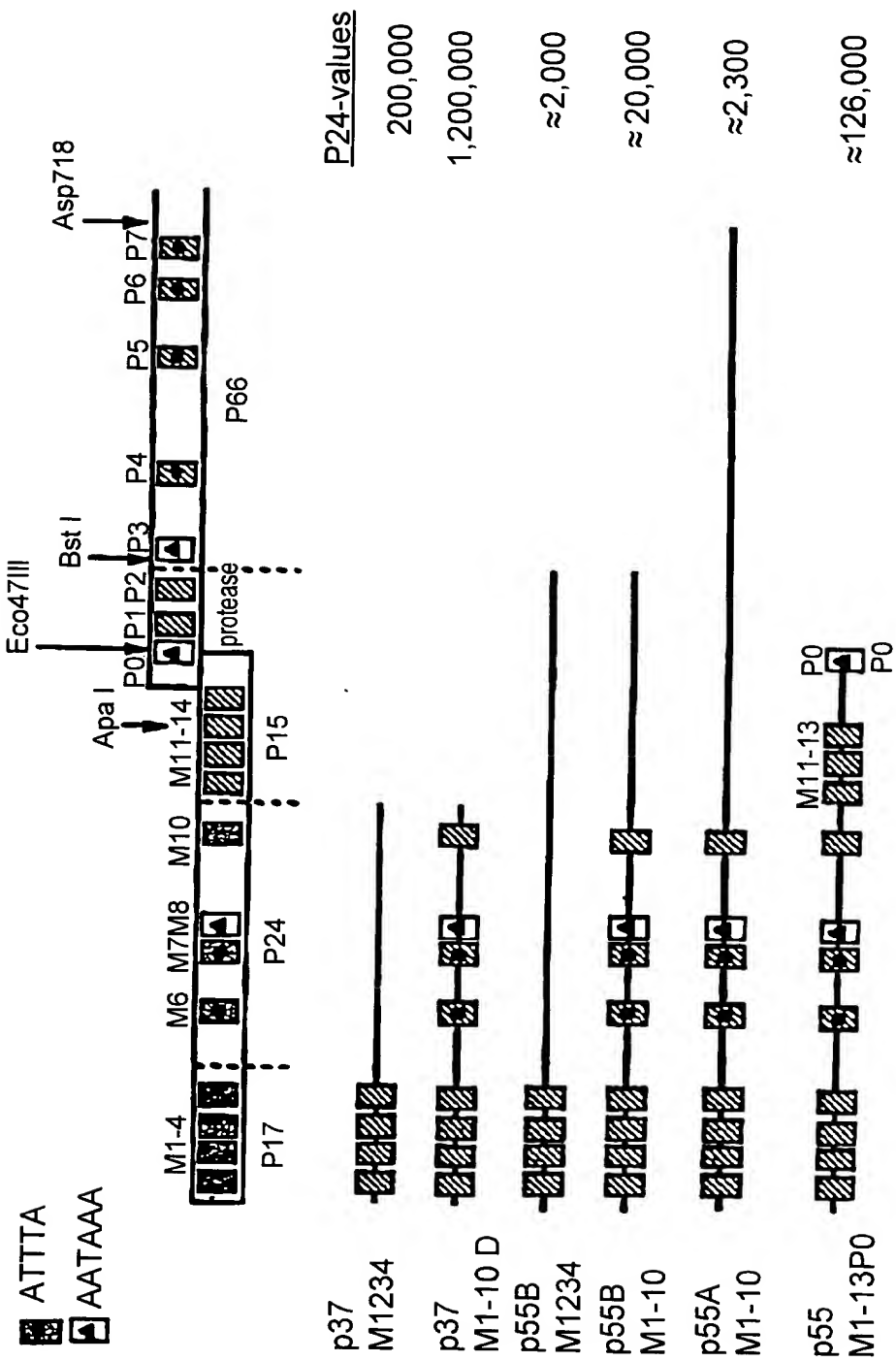



**Figure 6**

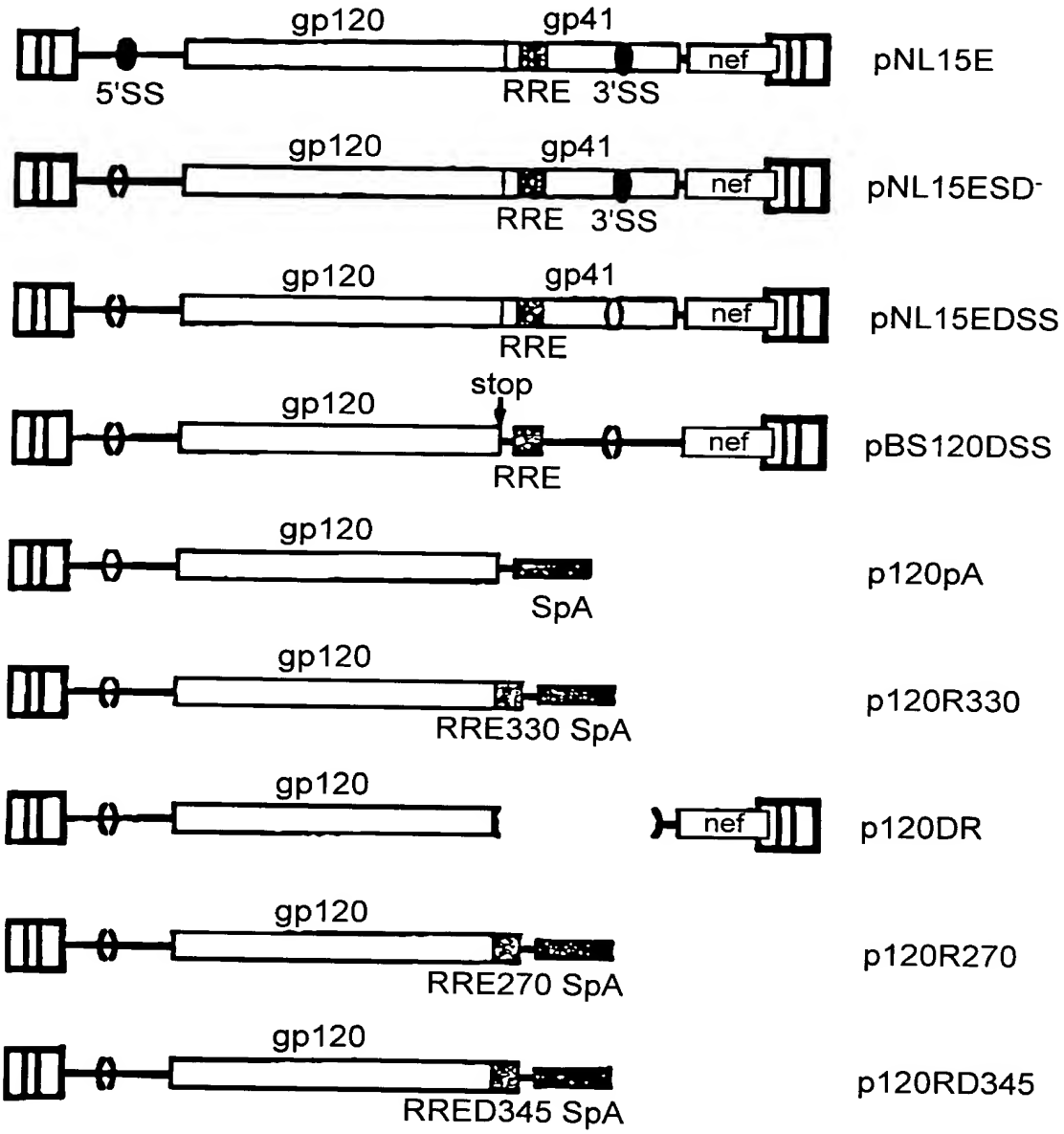
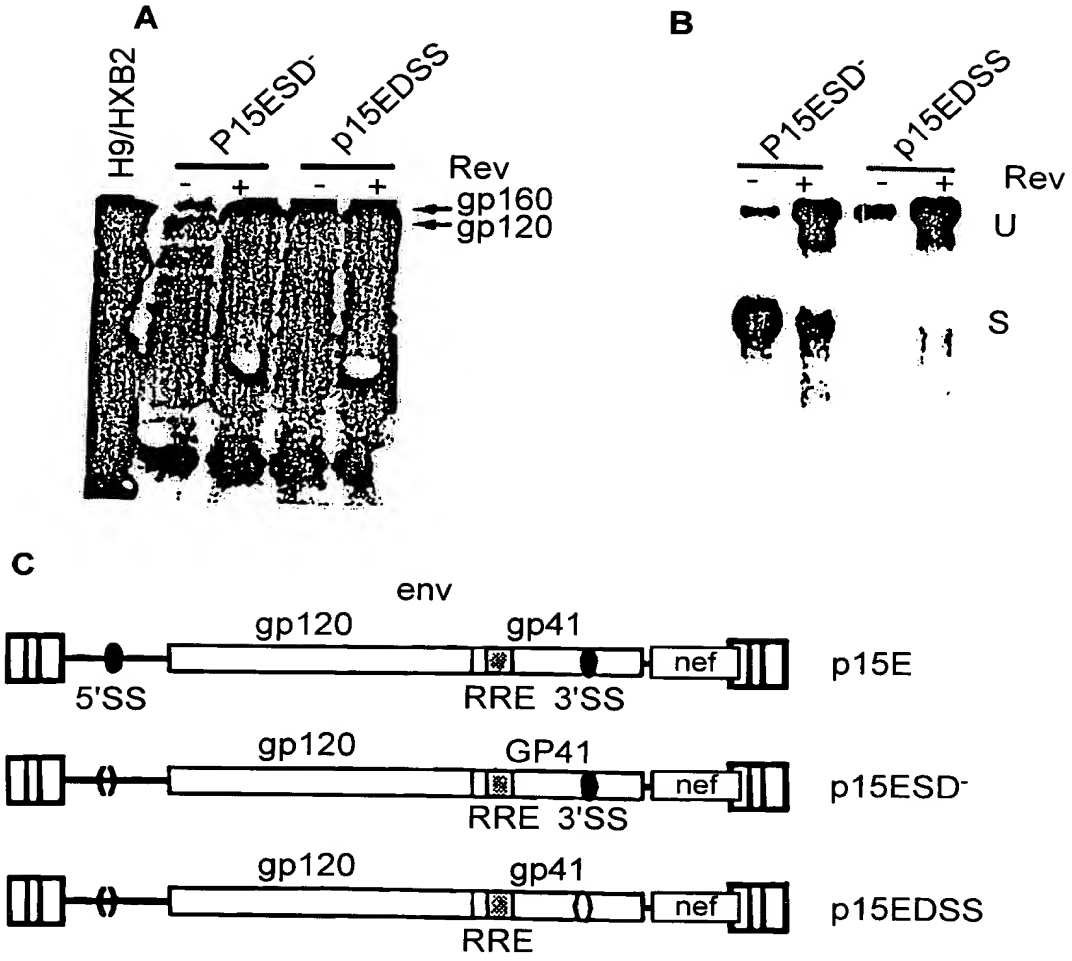



**Figure 7**

**Figure 8**



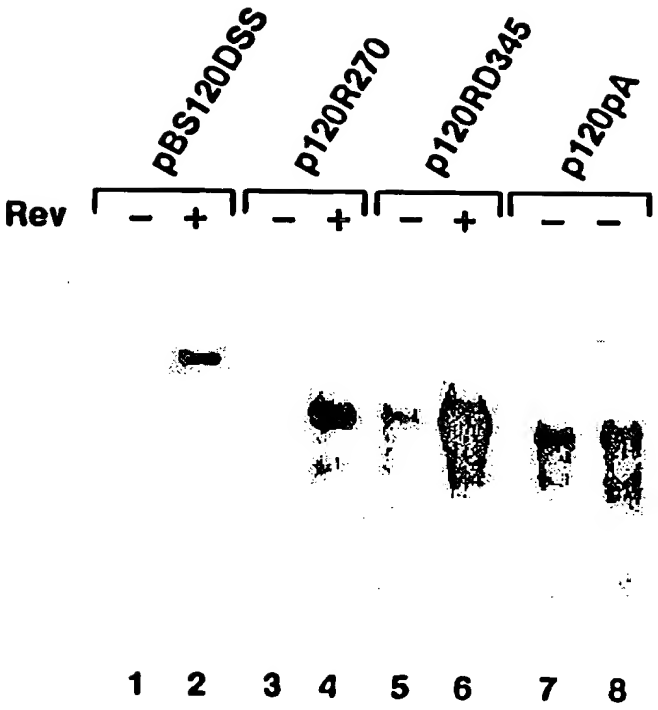
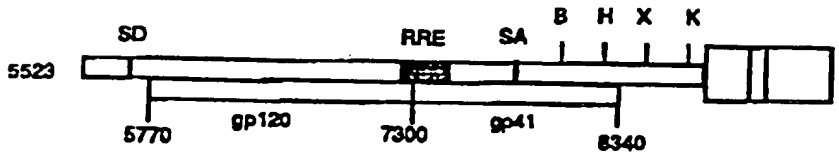



**Figure 9A**


Figure 9B

**Identification of INS regions within the env mRNA using the p19 vector.**




| | FRAGMENT | SIZE | | INS EFFECT |
|---|---|---|---|---|
| | A | 276 | 7684-7959 | none |
| | B | 234 | 7684-7884, 7927-7959 | none |
| | C | 323 | 7595-7884, 7927-7959 | 10 X |
| | D | 128 | 7939-8066 | none |
| | E | 478 | 7939-8416 | 10 X |
| | F | 362 | 8200-8561 | > 100 X |
| | G | 330 | 7266-7595 | 3-5X |
| E | | 668 | 5523-6190 | 10 X |

Figure 10

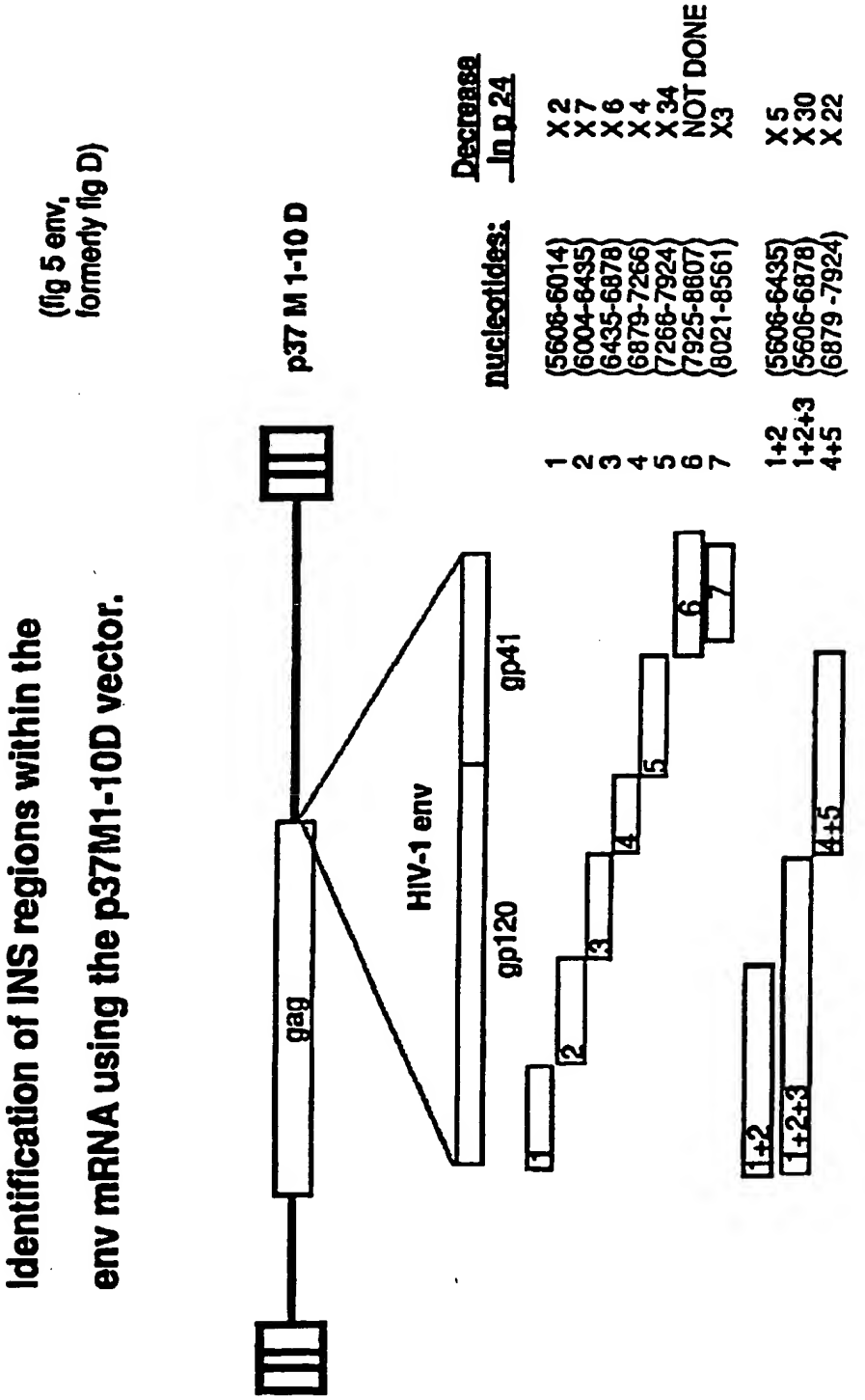
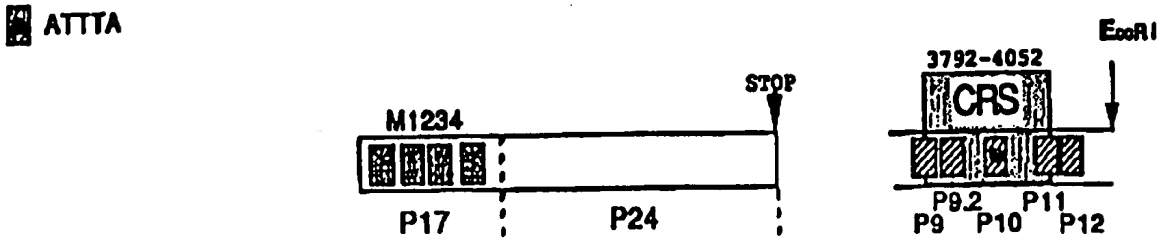



Figure 11

# Elimination of negative effects of CRS



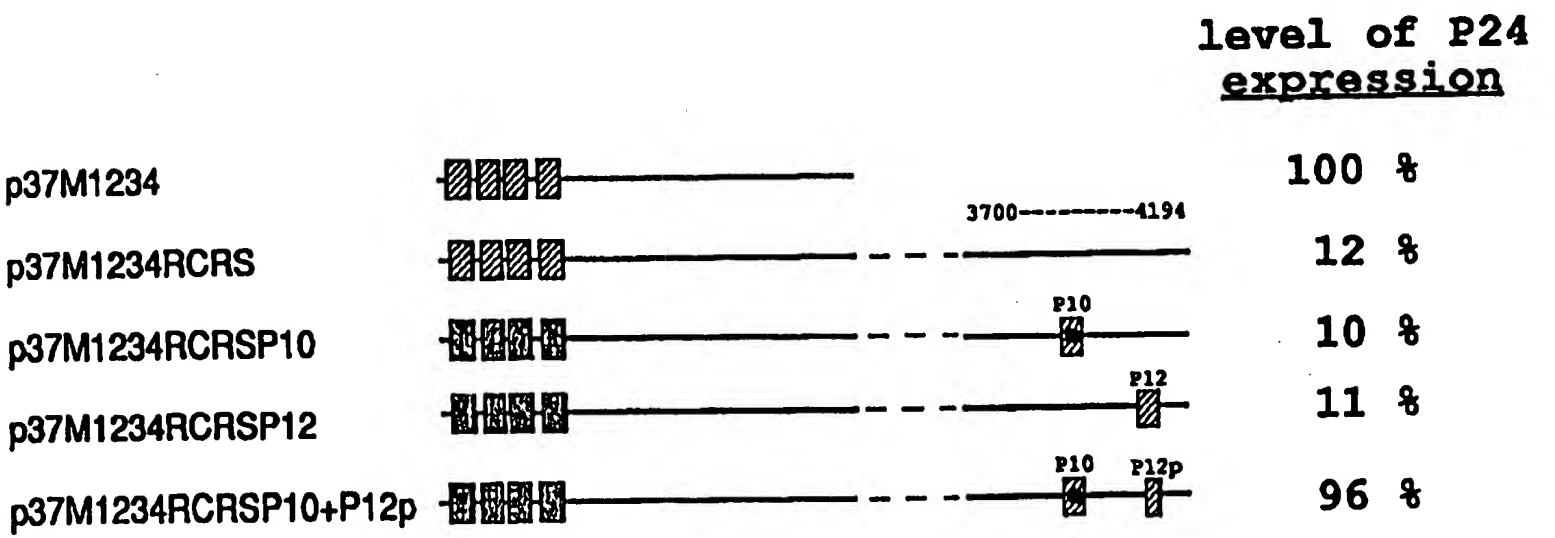




Figure 12

POINT MUTATIONS ELIMINATING THE NEGATIVE EFFECTS OF CRS IN THE pol REGION
(nucleotides 3700-4194) (SEQ ID NO:127)

GGTACCAGCACACAAAGGAATTGGAGGAAATGAACAAGTAGATAAATTAGTCAGTGCTGGAATCAGGAAAGTACTATTTT

TAGATGGAATAGATAAGGCCCAAGATGAACATGAGAAATATCACAGTAATTGGAGAGCAATGGCTAGTGATTTTAACCTG

CCACCTGTAGTAGCAAAAGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAGGAGAAGCCATGCATGGACAAGTAGA

CTGTAGTCCAGGAATATGGCAACTAGATTGTACACATTTAGAAGGAAAAGTTATCCTGGTAGCAGTTCATGTAGCCAGTG
g g c c g cc g g g g g

GATATATAGAAGCAGAAGTTATTCCAGCAGAAACAGGGCAGGAAACAGCATATTTTCTTTTAAAATTAGCAGGAAGATGG

CCAGTAAAAACAATACATACTGACAATGGCAGCAATTTCACCGGTGCTACGGTTAGGGCCGCCTGTTGGTGGGCGGGAAT
c g c a c t

CAAGCAGGAATTTGG

**Figure 13**

COMPLETE NUCLEOTIDE SEQUENCE OF p37M-1-10D
AND
AMINO ACID SEQUENCE OF $p37^{gag}$ PROTEIN (SEQ ID NO:129)

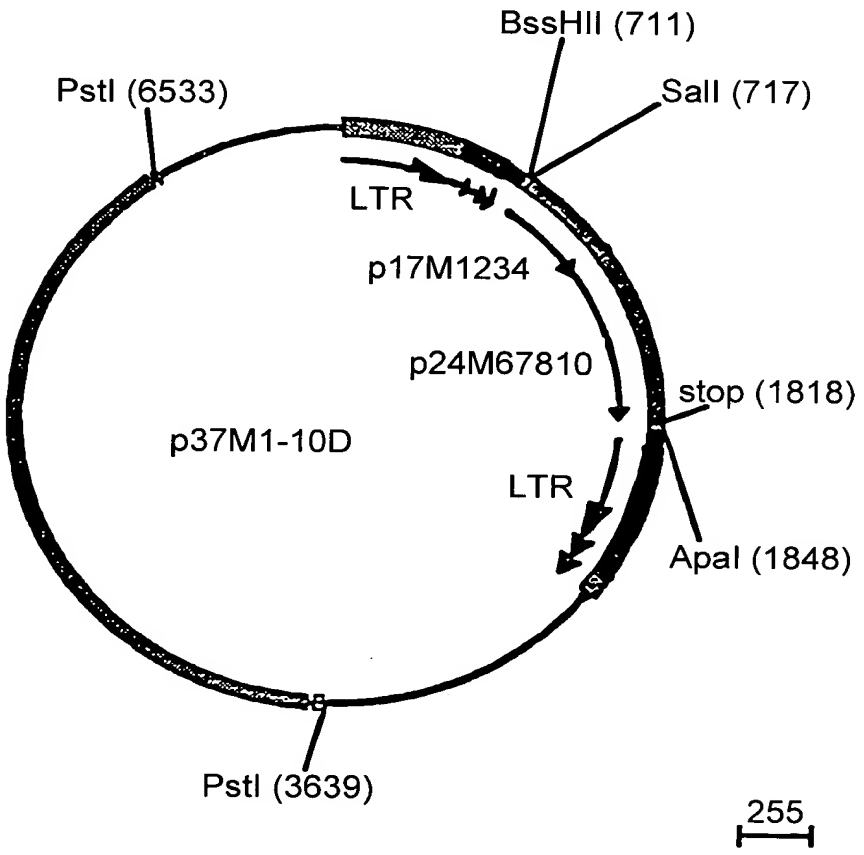



**Figure 14A**

```
   1 TGGAAGGGCT AATTTGGTCC CAAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA CACAAGGCTA

  71 CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC TGACCTTTGG ATGGTGCTTC

 141 AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA AATAAGGAGA GAAGAACAGC TTGTTACACC

 211 CTATGAGCCA GCATGGGATG GAGGACCCGG AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC

 281 ATTTCGTCAC ATGGCCCGAG AGCTGGATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG

 351 GGACTTTCCG CTGGGGACTT TCCAGGGAGG TGTGGCCTGG GCGGGACTGG GGAGTGGCGA GCCCTCAGAT

 421 GCTACATATA AGCAGCTGCT TTTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC

 491 TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCCT TGAGTGCTCA AAGTAGTGTG

 561 TGCCCGTCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC AGACCCTTTT AGTCAGTGTG GAAAATCTCT

 631 AGCAGTGGCG CCCGAACAGG GACTTGAAAG CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG
          BssHII (711)
 701 GCTTGCTGAAGCGCGCGTCGACAGAGAGATGGGTGCGAGAGCGTCAGTATTAAGCGGGGGAGAATTAGATCGATGG
                                    1►MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspArgTrp

 777 GAAAAAATTCGGTTAAGGCCAGGGGGAAAGAAGAAGTACAAGCTAAAGCACATCGTATGGGCAAGCAGGGAGCTAG
  17►GluLysIleArgLeuArgProGlyGlyLysLysLysTyrLysLeuLysHisIleValTrpAlaSerArgGluLeuG

 853 AACGATTCGCAGTTAATCCTGGCCTGTTAGAAACATCAGAAGGCTGTAGACAAATACTGGGACAGCTACAACCATC
  42►luArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCysArgGlnIleLeuGlyGlnLeuGlnProSe

 929 CCTTCAGACAGGATCAGAGGAGCTTCGATCACTATACAACACAGTAGCAACCCTCTATTGTGTGCACCAGCGGATA
  67►rLeuGlnThrGlySerGluGluLeuArgSerLeuTyrAsnThrValAlaThrLeuTyrCysValHisGlnArgIle

1005 GAGATCAAGGACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAAACAAGTCCAAGAAGAAGGCCCAGCAGG
  93►GluIleLysAspThrLysGluAlaLeuAspLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGlnA

1081 CAGCAGCTGACACAGGACACAGCAATCAGGTCAGCCAAAATTACCCTATAGTGCAGAACATCCAGGGGCAAATGGT
 118►laAlaAlaAspThrGlyHisSerAsnGlnValSerGlnAsnTyrProIleValGlnAsnIleGlnGlyGlnMetVa

1157 ACATCAGGCCATATCACCTAGAACTTTAAATGCATGGGTAAAAGTAGTAGAAGAGAAGGCTTTCAGCCCAGAAGTG
  11►lHisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysValValGluGluLysAlaPheSerProGluVal

1233 ATACCCATGTTTTCAGCATTATCAGAAGGAGCCACCCCACAGGACCTGAACACGATGTTGAACACCGTGGGGGGAC
  37►IleProMetPheSerAlaLeuSerGluGlyAlaThrProGlnAspLeuAsnThrMetLeuAsnThrValGlyGlyH

1309 ATCAAGCAGCCATGCAAATGTTAAAAGAGACCATCAATGAGGAAGCTGCAGAATGGGATAGAGTGCATCCAGTGCA
  62►isGlnAlaAlaMetGlnMetLeuLysGluThrIleAsnGluGluAlaAlaGluTrpAspArgValHisProValHi

1385 TGCAGGGCCTATTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACTACTAGTACCCTTCAG
  87►sAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAspIleAlaGlyThrThrSerThrLeuGln

1461 GAACAAATAGGATGGATGACAAATAATCCACCTATCCCAGTAGGAGAGATCTACAAGAGGTGGATAATCCTGGGAT
 113►GluGlnIleGlyTrpMetThrAsnAsnProProIleProValGlyGluIleTyrLysArgTrpIleIleLeuGlyL

1537 TGAACAAGATCGTGAGGATGTATAGCCCTACCAGCATTCTGGACATAAGACAAGGACCAAAGGAACCCTTTAGAGA
 138►euAsnLysIleValArgMetTyrSerProThrSerIleLeuAspIleArgGlnGlyProLysGluProPheArgAs
```

**Figure 14B**

```
1613 CTATGTAGACCGGTTCTATAAAACTCTAAGAGCTGAGCAAGCTTCACAGGAGGTAAAAAATTGGATGACAGAAACC
 163 pTyrValAspArgPheTyrLysThrLeuArgAlaGluGlnAlaSerGlnGluValLysAsnTrpMetThrGluThr

1689 TTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCATCCTGAAGGCTCTCGGCCCAGCGGCTACACTAGAAGAAA
 189 LeuLeuValGlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGlyProAlaAlaThrLeuGluGluM
                                                    stop (1818)   XbaI (1838)
1765 TGATGACAGCATGTCAGGGAGTAGGAGGACCCGGCCATAAGGCAAGAGTTTTGTAGGGATCCACTAGTTCTAGACT
 214 etMetThrAlaCysGlnGlyValGlyGlyProGlyHisLysAlaArgValLeu
          ApaI(1848)
1841 CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTTAAA

1911 AGAAAAGGGG GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC

1981 CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTCAGATAT CCACTGACCT

2051 TTGGATGGTG CTACAAGCTA GTACCAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAAG GAGAGAACAC

2121 CAGCTTGTTA CACCCTGTGA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTTAGA GTGGAGGTTT

2191 GACAGCCGCC TAGCATTTCA TCACGTGGCC CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC

2261 GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTTCCAGG GAGGCGTGGC CTGGGCGGGA CTGGGGAGTG

2331 GCGAGCCCTC AGATGCTGCA TATAAGCAGC TGCTTTTTGC CTGTACTGGG TCTCTCTGGT TAGACCAGAT

2401 CTGAGCCTGG GAGCTCTCTG GCTAACTAGG GAACCCACTG CTTAAGCCTC AATAAAGCTT GCCTTGAGTG

2471 CTTCAAGTAG TGTGTGCCCG TCTGTTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG

2541 TGTGGAAAAT CTCTAGCACC CCCCAGGAGG TAGAGGTTGC AGTGAGCCAA GATCGCGCCA CTGCATTCCA

2611 GCCTGGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG TATTAAATAT ATTTATACAT
2681 GGAGGTCATA AAAATATATA TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG
2751 CCGAGGCAGG TGGATCACCT GAGTTTGGGA GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCTTCTC
2821 TGTGTATTTT TAGTAGATTT TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAAACTGTT
2891 TTTCCTCTAC TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTTCT GTGATCAAAT GTGGTGGGAG
2961 AGGGAGGTTT TCACCAGCAC ATGAGCAGTC AGTTCTGCCG CAGACTCGGC GGGTGTCCTT CGGTTCAGTT
3031 CCAACACCGC CTGCCTGGAG AGAGGTCAGA CCACAGGGTG AGGGCTCAGT CCCCAAGACA TAAACACCCA
3101 AGACATAAAC ACCCAACAGG TCCACCCCGC CTGCTGCCCA GGCAGAGCCG ATTCACCAAG ACGGGAATTA
3171 GGATAGAGAA AGAGTAAGTC ACACAGAGCC GGCTGTGCGG GAGAACGGAG TTCTATTATG ACTCAAATCA
3241 GTCTCCCCAA GCATTCGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG
3311 ATGAAAGCGT AGGGAGTCGA AGGTGTCCTT TTGCGCCGAG TCAGTTCCTG GGTGGGGGCC ACAAGATCGG
3381 ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGCAAAA TATCTCAAGC
3451 ACTGATTGAT CTTAGGTTTT ACAATAGTGA TGTTACCCCA GGAACAATTT GGGGAAGGTC AGAATCTTGT
3521 AGCCTGTAGC TGCATGACTC CTAAACCATA ATTTCTTTTT TGTTTTTTTT TTTTTATTTT TGAGACAGGG
                                                    PstI (3639)
3591 TCTCACTCTG TCACCTAGGC TGGAGTGCAG TGGTGCAATC ACAGCTCACT GCAGCCCCTA GAGCGGCCGC
3661 CACCGCGGTG GAGCTCCAAT TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG TTTTACAACG
3731 TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC ATCCCCCTTT CGCCAGCTGG
3801 CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGCGCG
3871 AAATTGTAAA CGTTAATATT TTGTTAAAAT TCGCGTTAAA TTTTTGTTAA ATCAGCTCAT TTTTTAACCA
3941 ATAGGCCGAA ATCGGCAAAA TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTTCCA
4011 GTTTGGAACA AGAGTCCACT ATTAAAGAAC GTGGACTCCA ACGTCAAAGG GCGAAAAACC GTCTATCAGG
4081 GCGATGGCCC ACTACGTGAA CCATCACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA AAGCACTAAA
4151 TCGGAACCCT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG CGAACGTGGC GAGAAAGGAA
4221 GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGCGGT CACGCTGCGC GTAACCACCA
4291 CACCCGCCGC GCTTAATGCG CCGCTACAGG GCGCGTCCCA GGTGGCACTT TTCGGGGAAA TGTGCGCGGA
4361 ACCCCTATTT GTTTATTTTT CTAAATACAT TCAAATATGT ATCCGCTCAT GAGACAATAA CCCTGATAAA
```

**Figure 14C**

```
4431 TGCTTCAATA ATATTGAAAA AGGAAGAGTA TGAGTATTCA ACATTTCCGT GTCGCCCTTA TTCCCTTTTT
4501 TGCGGCATTT TGCCTTCCTG TTTTTGCTCA CCCAGAAACG CTGGTGAAAG TAAAAGATGC TGAAGATCAG
4571 TTGGGTGCAC GAGTGGGTTA CATCGAACTG GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTTCGCCCCG
4641 AAGAACGTTT TCCAATGATG AGCACTTTTA AAGTTCTGCT ATGTGGCGCG GTATTATCCC GTATTGACGC
4711 CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTCAG AATGACTTGG TTGAGTACTC ACCAGTCACA
4781 GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCTGC CATAACCATG AGTGATAACA
4851 CTGCGGCCAA CTTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACC GCTTTTTTGC ACAACATGGG
4921 GGATCATGTA ACTCGCCTTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC
4991 ACCACGATGC CTGTAGCAAT GGCAACAACG TTGCGCAAAC TATTAACTGG CGAACTACTT ACTCTAGCTT
5061 CCCGGCAACA ATTAATAGAC TGGATGGAGG CGGATAAAGT TGCAGGACCA CTTCTGCGCT CGGCCCTTCC
5131 GGCTGGCTGG TTTATTGCTG ATAAATCTGG AGCCGGTGAG CGTGGGTCTC GCGGTATCAT TGCAGCACTG
5201 GGGCCAGATG GTAAGCCCTC CCGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAC
5271 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTAA GCATTGGTAA CTGTCAGACC AAGTTTACTC
5341 ATATATACTT TAGATTGATT TAAAACTTCA TTTTTAATTT AAAAGGATCT AGGTGAAGAT CCTTTTTGAT
5411 AATCTCATGA CCAAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA
5481 AAGGATCTTC TTGAGATCCT TTTTTTCTGC GCGTAATCTG CTGCTTGCAA ACAAAAAAAC CACCGCTACC
5551 AGCGGTGGTT TGTTTGCCGG ATCAAGAGCT ACCAACTCTT TTTCCGAAGG TAACTGGCTT CAGCAGAGCG
5621 CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG GCCACCACTT CAAGAACTCT GTAGCACCGC
5691 CTACATACCT CGCTCTGCTA ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
5761 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA CGGGGGGTTC GTGCACACAG
5831 CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC
5901 TTCCCGAAGG GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC GCACGAGGGA
5971 GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA
6041 TTTTTGTGAT GCTCGTCAGG GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCGGCCTTT TTACGGTTCC
6111 TGGCCTTTTG CTGGCCTTTT GCTCACATGT TCTTTCCTGC GTTATCCCCT GATTCTGTGG ATAACCGTAT
6181 TACCGCCTTT GAGTGAGCTG ATACCGCTCG CCGCAGCCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG
6251 GAAGCGGAAG AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA TGCAGCTGGC
6321 ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAT GTGAGTTAGC TCACTCATTA
6391 GGCACCCCAG GCTTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT
6461 CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC
        PstI (6533)
6531 TGCTGCAGGG TCCCTAACTG CCAAGCCCCA CAGTGTGCCC TGAGGCTGCC CCTTCCTTCT AGCGGCTGCC
6601 CCCACTCGGC TTTGCTTTCC CTAGTTTCAG TTACTTGCGT TCAGCCAAGG TCTGAAACTA GGTGCGCACA
6671 GAGCGGTAAG ACTGCGAGAG AAAGAGACCA GCTTTACAGG GGGTTTATCA CAGTGCACCC TGACAGTCGT
6741 CAGCCTCACA GGGGGTTTAT CACATTGCAC CCTGACAGTC GTCAGCCTCA CAGGGGGTTT ATCACAGTGC
6811 ACCCTTACAA TCATTCCATT TGATTCACAA TTTTTTTAGT CTCTACTGTG CCTAACTTGT AAGTTAAATT
6881 TGATCAGAGG TGTGTTCCCA GAGGGGAAAA CAGTATATAC AGGGTTCAGT ACTATCGCAT TTCAGGCCTC
6951 CACCTGGGTC TTGGAATGTG TCCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTCACAGTG
7021 ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCACAATG GGCCGCCCTC CACGTGCACA TGGCCGGAGG
7091 AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCTTGGTG TGGAGGGAGG GACCAGCGCA
7161 GCTTCCAGCC ATCCACCTGA TGAACAGAAC CTAGGGAAAG CCCCAGTTCT ACTTACACCA GGAAAGGC
```

**Figure 14D**